

M., Rose, M., Rose, R., Stokes, R., Timney, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10Kb
plasmid inserts

TITLE JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Gen. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun-genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: K column: 21
Seq primer: CTTCTAAACACACCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19

FEATURES source

/organism="Mus musculus"
/strain="C57H1/6J"
/db_xref="taxon:10090"
/clone="GUSC1M0011E21"
/clone_lib="Mouse 10kb plasmid UMGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMW2Mv; Purified genomic DNA from M.
musculus (C57H1/6J) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMW2 (g1:14732114:gblAF129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10 Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 4 a 5 c 3 g 7 t

ORIGIN

Alignment Scores:
Prod. No.: 1,26e+03 Length: 19
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-856-070-25 (1-5) x A7108423 (1-19)

QY 1 MetLeuAraLeuGln 5
|||||
DB 16 ATGCTAGATTACAG 2

RESULT 2

AW423440/c
LOCUS SB66102.1 (50017) 54 bp mRNA linear EST 03-DEC-2001
DEFINITION Gm-c1015-4780 5', mRNA sequence.
ACCESSION AW423440
VERSION AW423440.1 GI:6951372
KEYWORDS EST
SOURCE soybean.
ORGANISM Glycine max

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids 1, Fabales, Fabaceae, Papilionoideae, Phaseolaceae,
Glycine.

REFERENCE AUTHORS

1 (bases 1 to 54)
Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Goryell, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kuraba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swalter, J., Gibbons, M., Fape, D., Harvey, N., Schurk
K., Ritter, E., Kohn, S., Shin, J., Jackson, Y., Cardenas, M., McCann
K., Waterston, R. and Willson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE JOURNAL COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available through: ResGen, Invitrogen Corp, 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cgen@resgen.com
Insert Length: 271 Std Error: 0.00
Seq primer: 40pp from Gibco.

FEATURES Source

1..54
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-4780"
/clone_lib="Gm-c1015"
/tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II XR; Site1: EcoRI; Site2:
XhoI; this cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR cDNA library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adaptors
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10 Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelidg."

BASE COUNT 11 a 7 c 16 q 20 t

Alignment Scores:
Prod. No.: 4.17e+03 Length: 54
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-856-070-25 (1-5) x AW423440 (1-54)

QY 1 MetLeuAraLeuGln 5
|||||
DB 27 ATGCTTAGACTTCAA 13

RESULT 3

BF456263
LOCUS BF456263
DEFINITION UI-M-B21-bkv-a-11-0-UI-s1 NIH/BMAP_MHI2.S1 Mus musculus cDNA clone
ACCESSION BF456263
VERSION BF456263.1 GI:11522432
KEYWORDS EST.
SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 66)
REFERENCE Honaldo,M.P., Lennon,G. and Soares,M.B.
AUTHORS Normalization and subtraction two approaches to facilitate gene
TITLE discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mst@mail.nih.gov
The sequence contained an oligo dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
hippocampus tissue cDNA Library Preparation. M.B. Soares from the
distribution: Researchers may obtain BMAP cDNA clones from REFARCH
GENETICS. It should be noted that Bento Soares is generating a
small number of additional specialized non redundant arrays of BMAP
cDNAs whose availability will be considered under appropriate and
limited collaborative arrangements
Seq primer: M13 Forward
POLVA-Yes.

FEATURES Location/Qualifiers
source
1..66
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="U1 M-B1-BKV-a-11-G-U1"
/clone_lib="NIH BMAP.MHI2_S1"
/seq_start="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73b-Pac (Pharmacia) with a modified
polylinker. Site 1 Not I, Site 2 Eco RI, The
NIH BMAP.MHI2_S1 library is a subtracted library derived
from NIH BMAP.MHI2. NIH BMAP.MHI2 is a library derived
from mouse hippocampus tissue. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_LIB="NIH BMAP.MHI2_S1"
TAG_SEQ="TAGTC"

BASE COUNT 19 a 16 c 16 q 15 t
ORIGIN
Alignment Scores:
Pred. No.: 5,25e+03 Length: 66
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-070-25 (1-5) x RF45524 (1-66)

QY 1 MetLeuArgLeuGln 5
LOCUS 66 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0193113F Mouse 10kb Plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0193113 F. DNA sequence.
ACCESSION A2417551
VERSION A2417551.1 GI:10541564
KEYWORDS GSS

SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 66)
REFERENCE Paudyal, A., Yari, A., Barber, M., Reardon, T., Durai, B., Hamil, C.,
Islam, H., Londeacre, S., Mahmoud, M., Mennen, E., Pedersen, T., Reilly,
J.M., Pose, M., Pose, P., Stokes, P., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Pm 308, Biomedical Building Research Bldg., 20 S. 2030 E., StG, UT
84112, USA
Tel: 801 585 5706
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: G193 Row: 1 Column: 13
Seq primer: CGTCTGTAAGGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 66.
FEATURES Location/Qualifiers
source
1..66
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0193113"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab_host="F. Coli strain XL10-Gold, T1-resistant, P-"
/note="Vector: pMD42hv: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrolytically sheared by repeated passage through a
0.305 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and 14
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid p1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent F. coli XL10 Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 14 a 20 c 17 q 15 t
ORIGIN
Alignment Scores:
Pred. No.: 5,25e+03 Length: 66
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-856-070-25 (1-5) x AZ417551 (1-66)

QY 1 MetLeuArgLeuGln 5
LOCUS 66 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0193113F Mouse 10kb Plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0193113 F. DNA sequence.
ACCESSION A2417551
VERSION A2417551.1 GI:10541564
KEYWORDS GSS

AA423006/c
LOCUS
DEFINITION
74 bp mRNA linear EST 16-OCT 1997
vc84a04.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:832878
5' similar to gb:108441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN
); mRNA sequence.
ACCESSION
VERSION
KEYWORDS
EST.
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 74)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gaisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, H.,
Teiching, H., Wylic, J., Lennon, G., Soares, H., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through HMI; contact the
IMAGE Consortium (info@image.hmi.gov) for further information.
M31:493094

```

seq primer: zmls1 rev2.ct from Amlersham
High quality sequence stop: 1.
location/Qualifiers
1. .74
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloc_xref="IMAGE:832878"
/clone_lib="Soares mouse NDMH"
/sex="male"
/lissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/Note "Vector: pT73B-pac (Pharmacia) with a modified
polylinker; Site_1, Not I, Site_2, Eco RI, 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
IGTAAAGATTTGAAGTGGAGTGGGCGGAACTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia) digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Patima
Bonaldo."
20 a 17 c 16 a 21 t
ORIGIN
Alignment Scores:
Pred. No.: 5,986-03 Length: 74
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Nearest Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
9 Gaps: 0
US-09-856-070-25 (1-5) x AA424006 (1-74)

```

Qy 1 MetLeuArgLeuGln 5
|||||
Db 43 ATGCTGGCGCTTCAA 29

RESULT 7
AA603472/C

LOCUS
DEFINITION
AA600472 74 bp mRNA linear EST 23-SEP-1997
vnt4h09.r1 knowles solter mouse blastocyst B1 Mus musculus cDNA
clone IMAGE:1004417 5' similar to gb-104441 Cytoschrome C OXIDASE
POLYPEPTIDE III (HUMAN); mRNA sequence.

ACCESSION
AA600472 1 GI:2434067

VERSION
AA600472.1

KEYWORDS
EST.

ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 74)

REFERENCE
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, L.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, P., Wilson, P. and
Waterston, R.

TITLE
The WashU-HMI Mouse EST Project

JOURNAL
Unpublished (1996)

COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through HMI. Contact the
IMAGE Consortium (info@image.lnlnl.gov) for further information
MGI:568633

Trace considered overall poor quality
High quality sequence stop: 1.
Location/Qualifiers
1..74
/organism="Mus musculus"
/strain="c57BL/6J x PRA/21 F1"
/db_xref="taxon:10090"
/clone="IMAGE:1004417"
/clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="PH10B"
/note="Organ: embryo; Vector: pSCK1, Site: l. Notif.
Site: 2. Salt. Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: Salt(dT):
5'-CGCTGACGCGGACGCTTTTITTTTTTTT-3'. cDNAs were
cloned into the NotI/SalI sites of a pSCK1 vector (Life
Technologies). Two different size selections: B1 (larger
inserts) and B3."

BASE COUNT
25 a 16 c 12 g 21 t

ORIGIN
|||||

Alignment Scores:
Pred. No.: 5.98e+03 Length: 74
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-856-070-25 (1-5) x AA600472 (1-74)

QY 1 MetLeuArgIleuGln 5
|||||

Db 53 ATGTTGGGCTTCAA 49

RESULT 8
BF314574
LOCUS
BF314574 76 bp mRNA linear EST 21-NOV-2000
601901585F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130781 5',
mRNA sequence.

ACCESSION
BF314574

VERSION
BF314574.1 GI:11262796

KEYWORDS
EST.

SOURCE
ORGANISM
Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 76)

REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

JOURNAL

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rpubbs@email.nih.gov
Tissue Procurement: ATCC

CDNA library preparation: Ling Hong/Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnlnl.gov
Plate: LLM1027 row: 1 column: 22
High quality sequence stop: 76.

FEATURES
source
1..76
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4130781"
/clone_lib="NIH-MGC_19"
/tissue_type="neuroblastoma"
/lab_host="PH10B (phage-resistant)"
/note="Organ: brain; Vector: pSCK1, Site: l. XhoI, Site: 2.
EcoRI; cDNA made by oligo dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(C). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

BASE COUNT
21 a 18 c 25 g 12 t

ORIGIN
|||||

Alignment Scores:
Pred. No.: 6.17e+03 Length: 76
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-070-25 (1-5) x BF314574 (1-76)

QY 1 MetLeuArgIleuGln 5
|||||

Db 49 ATGTTGGGCTTACAG 35

RESULT 9
N71860
LOCUS
N71860 78 bp mRNA linear EST 15-MAR-1996
Y234001.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:284929 5' similar to gb187912:HUMAN:NIH562 Human carcinoma
cell-derived Alu PNA transcrip; (PNA); gb:269556 INTERLEUKIN-6
RECEPTOR PPTCTPSP (HUMAN); mRNA sequence.

ACCESSION
N71860
VERSION
N71860.1 GI:1228572

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 78)

REFERENCE
Hillier, L., Lennon, G., Becker, M., Ronaldo, M.F., Chiapelli, R.,
Chissoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins,
M., Hillman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rink, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, P. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags

JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGe Consortium (info@image.lnl.gov) for further information.

Seq primer: m3 -40 forward
High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..78
/organism="Homo sapiens"
/db_xref="GDB:1892046"
/db_xref="taxon:9606"
/clone="IMAGe:284929"
/issue_lib="Morton Fetal Cochlea"
/issue_type="Cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLK cells (Kanamycin resistant)"
/note="Organ: ear; Vector: pBluescript SK⁺ Site:1: EcoRI;
Site:2: XhoI; Reference: Genomics 23, 42-50 (1994) cloned
unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
37% of inserts 0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAF
X8 Vector: Library constructed by N. Robertson, C. Morton
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CCGCAGTTTTTTTTTTT 3'

BASE COUNT 14 a 22 c 23 g 19 t
ORIGIN

Alignment Scores:
Pred. No.: 6,46e+03 Length: 78
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US 09 856 070-25 (1-5) x N71860 (1-78)

QY 1 MetLeuArcLeuGln 5
|||||

DB 62 ATCTTCAGG-TCGAC 48

RESULT 10

HH218187
LOCUS HH218187.1 GI:16810650
DEFINITION HH218187.1 linear GSS 08-NOV 2001
sequence.

ACCESSION HH218187.1 GI:16810650

VERSION HH218187.1

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 82)

AUTHORS Walbot V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL unpublished (2001)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post ligation sequence from source sequence.
Plate: 1006077 row: 27

FEATURES

Source

Class: transposon-tagged.

Location/Qualifiers

1..82
/organism="Zea mays"
/cultivar="mixed background W23/A186/H71"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/issue_type="leaf"
/dev_stage="adult"
/lab_host="DH10H"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site:1: BamHI; Site:2: BclII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BclII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT 17 a 21 c 20 g 24 t
ORIGIN

Alignment Scores.

Pred. No.: 6,73e+03 Length: 82
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-856-070-25 (1-5) x HH218187 (1-82)

QY 1 MetLeuArcLeuGln 5

DB 46 ATGTCGTCGAC 50

RESULT 11

AA438242/c

LOCUS AA438242

DEFINITION

IMAGe:743449 5' similar to qf:LOH441 CYTOCHROME C OXIDASE
POLYPEPTIDE III (HUMAN); mRNA sequence.

ACCESSION AA438242

VERSION AA438242.1 GI:2143156

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 95)

AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Pfeisinger B., Wylicke P., Lennon G., Soares H., Wilson R. and
Waterston R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGe Consortium (info@image.lnl.gov) for further information.
MGI:477757
Seq primer: -40m13 fwd. FI from Amersham.

FEATURES

Source

Location/Qualifiers

1..95


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Pred. No.: 8.45e+03 Length: 99
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US 09 856-070-25 (1-5) x BF448833 (1-99)

OY 1 MotileuArgleuGln 5
Db 99 ATGTAAGACTGAG 85

RESULT 14
AW545146
LOCUS AW545146 100 bp mRNA linear EST 31-AUG-2000
DEFINITION C0189A10-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus
ACCESSION AW545146
VERSION AW545146.1 GI:7187469
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 100)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grabovac
M.J., Pantano,S., Sano,Y., Flao,Y., Nayyaraja,R., Doi,H., Wood,W.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16): 9127-9132 (2000)
20481348
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cduadlusn@rc.nia.nih.gov
Plate: C0189 row: A column: 10
Seq primer: -21M13 Forward
High quality sequence stop: 100
POLYA-Yes.

FEATURES
Location/Qualifiers
1..100
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="niafst:C0189A10-3"
/db_xref="taxon:10090"
/clone="C0189A10"
/clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA
Library"
/sex="unknown"
/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
/Note="Vector: pSPORI1 (Gibco/BRL Life Technologies);
Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
5 EPC. The double stranded cDNA was synthesized by
Gibco's kit with an Oligo(dT) primer (NotI primer-adaptor
from Gibco/BRL)
15'-pGATTAATGCTTAAATAGTGGAGAGGAGGCGCTTTTTTTTTT-3'
from 0.8ug of mRNA. The double-stranded cDNAs were
treated with T4 DNA polymerase and purified by
ethanol-precipitation. The cDNAs were ligated to
long-linker-lin-Sal3 (include SalI sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by centrifugation 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Taq
polymerase. Then, the cDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with SalI and NotI enzymes then, the cDNAs were
size selected by Gibco's Size Fractionation Column. The
cDNAs were cloned into SalI/NotI site of pSPORI1 plasmid
vector. The DH10B E. coli host was transformed with the

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ligation mixture by chemical method. The library was
constructed by Xiaohong Wang."

BASE COUNT 35 a 18 c 21 g 26 t
ORIGIN

Alignment Scores:
Pred. No.: 8.44e+03 Length: 100
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-856-070-25 (1-5) x AW545136 (1-100)

OY 1 MotileuArgleuGln 5
Db 67 ATGCTGCGGCTTCAA 81

RESULT 15
AW863056
LOCUS AW863056 105 bp mRNA linear EST 22 MAY 2000
DEFINITION MK2-SN0007 100500-057-009 SN0007 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW863056
VERSION AW863056.1 GI:7997106
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105)
Nagai,M.A., da Silva,W.J.R., Zago,M.A., Hordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jenequel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof Antonio Prudente 180, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=st2-MK2-SN0007-100
500-007-009&t3=2000-05-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 105.
High quality sequence stop: 105.

FEATURES
Location/Qualifiers
1..105
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="SN0007"
/dev_stage="Adult"
/Note="Organ: stomach_tumor; Vector: puc18; Site1: SmaI;
Site2: SmaI; A mini library was made by cloning products
derived from ORFIES PCR (U.S. letters patent application
No. 196,716 - Ludwig Institute for Cancer Research)
provides into the puc18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 34 a 29 c 20 g 22 t
ORIGIN

Alignment Scores:

```


Pred. No.: 8.93e+03 Length: 105
 Score: 23.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-856-070-25 (1-5) x AW863056 (1-105)

QY 1 MetLeuArgLeuGln 5

DB 37 ATGCTAGAGACTTCAG 51

Search completed: January 16, 2003, 21:37:11
 Job time : 665.571 secs

